

PCT09

RAW SEQUENCE LISTING

DATE: 06/22/2001

PATENT APPLICATION: US/09/674,330A

TIME: 12:11:11

Input Set : A:\ES.txt

Output Set: N:\CRF3\06222001\I674330A.raw

3 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.
 5 <120> TITLE OF INVENTION: A NOVEL POLYPEPTIDE, A CDNA ENCODING THE POLYPEPTIDE AND UTILIZATION

6 THEREOF

8 <130> FILE REFERENCE: Q61536

10 <140> CURRENT APPLICATION NUMBER: 09/674,330A

11 <141> CURFENT FILING DATE: 2000-10-30

13 <150> PRIOR APPLICATION NUMBER: JP 10-119731

14 <151> PRIOR FILING DATE: 1998-04-28

16 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02283

17 <151> PRIOR FILING DATE: 1999-04-28

19 <160> NUMBER OF SEQ ID NOS: 12

21 <170> SOFTWARE: PatentIn version 3.0

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 1344

25 <212> TYPE: DNA

26 <213> ORGANISM: Mus musculus

28 <400> SEQUENCE: 1

29 atgacaggat taaaaaggat actcaactgtt accatcttgg cactctggct tccacatcct	60
31 gggatgcaac agcagcagtg cacaaacggc tttagacctg accgccagtc aggacagtgt	120
33 ctatgatattg atgaatgccg gaccatccct gaggetttgt gtggggacat gatgtgtgtc	180
35 aaccagaatg ggggtatatt gtgcatecct cgaaccaacc cagtgtatcg agggccttac	240
37 tcaaatccct actctacatc ctaactcagc ccatacccag cagcgccccc accagtacca	300
39 gcttccaact accccaagat ttcaaggcct cttgtctgac gctttgggta tcagatggat	360
41 gaaggcaacc agtgtgtgga tgtggacgag tgtgcaacag actcaacca gtgcaacctt	420
43 accagatctt gtatcaaac tgaaggaggt tacacctgct cctgcaccga tgggtacttg	480
45 cttctgggaag ggcagtgctt agatattgat gaatgtcgct atggttactg ccagcagctc	540
47 tgtgcaaatg ttccaggatc ctattcctgt acatgcaacc ctggtttcac cctcaacgac	600
49 gatggaaggt cttgccaaga tgtgaacgag tgcgaaactg agaatccctg tgttcagacc	660
51 tgtgtcaaca cctatggctc ttcatctgc cgtgttgacc caggatatga acttgaggaa	720
53 gatggcatte actgcagtgat tatggacgag tgcagcttct ccgaqttcct ctgtcaaac	780
55 gagtgtgtga accagccggg ctcatacttc tgcctgtgac ctccaggcta cgtcctgttg	840
57 gatgataacc gaaqctgcca ggataatcaat gaatgtgagc accgaaacca cactgtgacc	900
59 tcaatgcaga cttgtatcaa tctacaaggc ggcctcaaat gtattgatcc catcagctgt	960
61 gagtagcctt atctgtgat tggtagaaac cgtgttatgt gtccgtgtga gcacaccaga	1020
63 tgcagagacc agccatccac catcctgtat cgggacatgg atgtgggtgc aggaacgtcc	1080
65 gttcctgtctg acatcttcca gatgcaagca acaaccgat accctgggtg ctattacatt	1140
67 ttcagatcca aatctggcaa cgaaggctga gagttctata tgcggcaaac agggcctatc	1200
69 atgcccacc tggatgatga acgcccacat aaagggcctc gggacatcca gctggaactg	1260
71 gagatgatca ctgtcaaac tgtcatcaac ttcagaggca gctccgtgat ccgaactgag	1320
73 atatatgtgt ccagtatccc gttc	1344

76 <210> SEQ ID NO: 2

77 <211> LENGTH: 2233

78 <212> TYPE: DNA

79 <213> ORGANISM: Mus musculus

81 <220> FEATURE:

82 <221> NAME/KEY: misc_feature

83 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse embryonic heart

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86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <223> OTHER INFORMATION: "n" may be either a, c, g or t
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92 <221> NAME/KEY: CDS
93 <222> LOCATION: (75)..(1418)
95 <220> FEATURE:
96 <221> NAME/KEY: sig_peptide
97 <222> LOCATION: (75)..(143)
99 <220> FEATURE:
100 <221> NAME/KEY: mat_peptide
101 <222> LOCATION: (144)..()
103 <400> SEQUENCE: 2
104 aatttgggcac gagccccagt cccacccgcag agcctgcctt cctcgcgctcg cttctctctcc 60
106 cgcgcacatctt ggat atg cca gga tta aaa agg ata ctc act gtt acc atc 110
107 Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile
108 -20 -15
110 ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag cag tgc aca 158
111 Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr
112 -10 -5 -1 1 5
114 aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat 206
115 Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp
116 10 15 20
118 gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc 254
119 Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
120 25 30 35
122 aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat 302
123 Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr
124 40 45 50
126 cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac 350
127 Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr
128 55 60 65
130 cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca 398
131 Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser
132 70 75 80 85
134 agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag 446
135 Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln
136 90 95 100
138 tgt gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct 494
139 Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro
140 105 110 115
142 acc cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc acc 542
143 Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr
144 120 125 130
146 gat ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt 590
147 Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys
148 135 140 145
150 cgc tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat 638
151 Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr

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cca
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218 cag tat ccg ttc tgaagcctctg gctaaggcct ctgacaactgc ctttcaccag      1458
219 Gln Tyr Pro Phe
220                               425
221 caaccgagqja cgggaggaga aaggaaacca gcaagaatga gagcgagaca gacattgcac      1518
222 ctttctctgt gaatactctc tgggggcate agcctagcat cttgacccat atctgtacta      1578
223 ttgcagatgg tcaacttgaa ggacacccctg ccttcagttc ctatgatga gttatccaaa      1638
224 agtggttcac ttagcccttg atatgaggtt gccagtgact cttcaaaagcc ttccatttat      1698
225 ttccatcggt ttataaaaaa gaaaatagat tagatttgcg ggggtatgag tcttcgaagg      1758
226 ttcaaaagac tgagtggcct gctctcaact cttctctctc ttctccatc tcttgcgcga      1818
227 ttgctgcttt gcaaaagtc tcatgggctc gtgggaaatg ctgggaatag ctagtcttct      1878
228 tcttgcctgt tctgagaagg ctatgggaac acaccacagc aggatcgaaq gtttttatag      1938
229 agtctatttt aaaatcacat ctgggtatttt cagcataaaa gaaatttttag ttgtctttaa      1998
230 aatttgatg agtggtttaac cttttcttat tcattttgag gctttctaaa gtggtagaat      2058
231 tcttccaaa ggcttcagat acatgttatg ttcagtcctt ccaacctcat ctttctctgc      2118
W--> 244 atcttagccc agtttttacg aagaccctt aatcatgctt tnttaagagt ttttacccaa      2178
245 ctgcgttggg agacagaggt atccagaact attaaataat tgaagaaaaa aaaaa      2233
249 <210> SEQ ID NO: 3
250 <211> LENGTH: 448
251 <212> TYPE: PRT
252 <213> ORGANISM: Mus musculus
253 <220> FEATURE:
254 <221> NAME/KEY: misc_feature
255 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse embryonic heart
258 <400> SEQUENCE: 3
260 Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Trp
261                               -20                               -15                               -10
264 Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp
265                               -5                               -1    1                               5
268 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
269 10                               15                               20                               25
272 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
273                               30                               35                               40
276 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
277                               45                               50                               55
280 Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
281                               60                               65                               70
284 Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val
285 75                               80                               85
288 Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val
289 90                               95                               100                               105
292 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
293                               110                               115                               120
296 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
297                               125                               130                               135
300 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
301                               140                               145                               150
304 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
305 155                               160                               165
308 Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val

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309 170          175          180          185
312 Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
313          190          195          200
316 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
317          205          210          215
320 Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
321          220          225          230
324 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser
325          235          240          245
328 Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
329 250          255          260          265
332 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr
333          270          275          280
336 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys
337          285          290          295
340 Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala
341          300          305          310
344 Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
345          315          320          325
348 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
349 330          335          340          345
352 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
353          350          355          360
356 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
357          365          370          375
360 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile
361          380          385          390
364 Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
365          395          400          405
368 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
369 410          415          420          425
372 <210> SEQ ID NO: 4
373 <211> LENGTH: 423
374 <212> TYPE: PRT
375 <213> ORGANISM: Mus musculus
377 <400> SEQUENCE: 4
379 Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
380 1          5          10          15
382 Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
383          20          25          30
385 Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
386          35          40          45
388 Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
389          50          55          60
391 Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
392 65          70          75          80
394 Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
395          85          90          95
397 Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 06/22/2001

PATENT APPLICATION: US/09/674,330A

TIME: 12:11:12

Input Set : A:\ES.txt

Output Set: N:\CRF3\06222001\I674330A.raw

L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:1029 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11

L:1029 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11